

	M	A	P	P	A	A	R	L	A	L	L	11	
GTCGACCA	CGTCCG	CCACG	GTCCG	CCC	ATG	GCG	CGC	GCC	GCC	CTC	GCC	CTG	66
S	A	A	L	T	A	R	P	A	P	S	G	L	31
TCC	GCC	GCG	GCG	CTC	ACG	CTG	GCG	CCC	GCG	CCT	AGC	CCC	126
P	E	C	F	T	A	N	G	A	D	Y	R	G	51
CCC	GAG	TGT	TTC	ACA	GCC	AAT	GGT	GCG	GAT	TAT	AGG	GGA	186
Q	G	G	K	P	C	L	F	W	N	E	T	F	71
CAA	GCG	GGG	AAG	CCA	TGT	CTG	TTT	TGG	AAC	GAG	ACT	TTC	246
K	Y	P	N	G	E	G	L	G	E	H	N	Y	91
AAA	TAC	CCC	AAC	GGG	GAG	GGG	CTG	GGT	GAG	CAC	AAC	TAT	306
D	V	S	P	W	C	Y	V	A	E	H	E	D	111
GAC	GTG	AGC	CCC	TGG	TGC	TAT	GTG	GCA	GAG	CAC	GAG	GAT	366
E	I	P	A	C	Q	M	P	G	N	L	G	C	131
GAG	ATA	CCT	GCT	TGC	CAG	ATG	CCT	GGA	AAC	CTT	GGC	TGC	426
P	P	L	T	G	T	S	K	T	S	N	K	L	151
CCT	CCT	CTA	ACT	GGC	ACC	AGT	AAA	ACG	TCC	AAC	AAA	CTC	486
F	C	R	S	Q	R	F	K	F	A	G	M	E	171
TTT	TGT	CGG	AGT	CAG	AGG	TTC	AAG	TTT	GCT	GGG	ATG	GAG	546

Fig. 1A

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

Fig. 1B

P A V N Q T V A E V I T E Q A N L S V S	351
CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC	1086
A A R S S K V L Y V I T T S P S H P P Q	371
GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG	1146
T V P G S N S W A P P M G A G S H R V E	391
ACT GTC CCA GGT AGC AAT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA	1206
G W T V Y G L A T L L I L T V T A I V A	411
GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC ACA GTC ACA GCC ATT GTA GCA	1266
K I L L H V T F K S H R V P A S G D L R	431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG	1326
D C H Q P G T S G E I W S I F Y K P S T	451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT	1386
S I S I F K K K L K G Q S Q Q D D R N P	471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC	1446
L V S D *	476
CTT GTG AGT GAC TAA	1461

Fig. 1C

AAACCCACTGTGCCTAGGACTTGAAGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTTCTTCTC 1540  
 TGACAGACTCTTCCCTCCTCTCCCTCTGCTCGGCTCTTCCGGAACCTCCTCTACAGACTAGGAAGAGGCACCT 1620  
 GCTGCCAGGGCAGGACAGCTGGATTCTCCTGCTT 1657

**Fig. 1D**

GTCGACCCACGGTCCGCCCGGCTCCCGGTGCTGCCCTCTGCCCCGGCGCGCGGGGTCCCGCACTGACGGCC 79

M A P P A A R L A L L S A A A L T L A 19  
 C ATG GCG CCG CCC GCC GCG CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137

A R P A P G P R S G P E C F T A N G A D 39  
 GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197

Y R G T Q S W T A L Q G G K P C L F W N 59  
 TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257

E T F Q H P Y N T L K Y P N G E G L G 79  
 GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317

E H N Y C R N P D G D V S P W C Y V A E 99  
 GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

**Fig.1E**

H	E	D	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917

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Fig.1F

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

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Fig.1G

V	R	V	N	K	M	T	A	I	P	S	*	
GTC	AGA	GTC	AAC	AAG	ATG	ACC	GCA	ATC	CCC	TCG	TGA	1493
GTG	ACT	GAAG	CCCC	CAC	CGCT	GCAT	GAG	GGCT	CCG	CTCC	AAGCT	CGAGTTTGCTCCCCCTGAGTTCTCCTCTGATGAGTTC 1572
CC	TG	CTT	CCC	ATT	CAC	CAC	ATCT	CTTT	GG	AGC	ACCT	TGCTTTTAGAGGCAGCCCCAGCCTGGGATCCTCCATCACAT 1651
GT	ACC	AGC	CTG	CTG	CTG	CTGG	GATGG	TAA	GAC	AGAC	AGCT	GGACCTGACTCCAGAAGA 1730
CT	CTT	GGG	TGG	TGG	AGG	TAT	AGT	GTAG	GTAG	TTT	CTCT	CTCTTGTCCACATACAGATCGGTTTC 1809
CC	CT	GTCT	TTT	A	CAG	TTT	GCA	TAG	ACC	AGACT	GAA	AACTGTCAGGTTTCTAGGCTGGCCTGGTTCCCCACTAAGA 1888
GT	GC	ATT	GG	CC	CT	AG	AG	CC	CC	AG	CTT	CTCTGCTGCCAACTACCATGTGTCTATCT 1967
AG	TCC	GAG	GGG	ACT	GAG	AG	CG	CC	AC	AC	AGAT	GTCTTTCTAGAGGGTCTCTTTTAGTACCCACTGACCAATGG 2046
GG	CA	AGC	CT	GAG	GA	TTG	TCC	ATG	GA	ATG	GA	ATGAACTTCCCTGGATACCTAGACTTAAGTACGCC 2125
TAG	CC	CT	CA	AG	TAG	TTG	CC	AT	CA	GA	AT	TCCTGTCTCAGCCCCAAGCCTGTAGCCTAG 2204
AG	CT	GGG	CT	GTAG	CT	GGG	CTGTAG	CT	GGG	CTGTAG	CA	CAGAGCTGGGCTGTAGCCTAGAGC 2283
TGG	GG	CTGTAG	CAC	AG	CTGGG	CTGTAG	CTGGG	CTGTAG	CA	CAG	AGCTGGG	CTGTAGCACAGAGCTGG 2362
GG	CTGTAG	CC	TAG	AGCTGGG	CTGTAG	CTGGG	CTGTAA	CTCAG	CG	ATCA	AGAGCTTGCTTTGTATACATCG 2441	
GAC	CT	AG	GTCT	ATCC	AG	ACTAT	CA	GA	AGG	TGG	AG	AAAAAGACTGCACCATAGCATCGGGCAGCATCTGTGG 2520
TT	CT	AC	GTG	GTCA	TTTT	AA	AGC	AGATCA	AA	ACTAC	CGG	AGTTTGTCTCTTGTCCCTTATCATGGGAGC 2599
AG	AG	TAG	GA	GTAA	GG	CTCT	GTCT	ATTG	CT	CCCC	AGACAGGGCAGGCAAAAGTCAAGCTTGGGA	ACTGGA 2678
GAT	CC	TCC	CAG	AAA	AGCTG	CAAG	ATTG	AG	AC	CC	AG	CTGCAGTTGGGAGAGAGGCCCATCCCCGACTGAGAAATC 2757
CT	G	AG	CTGGA	AGTGG	CTTT	GT	CAG	AG	CTGT	CCC	TGAAGGTAGACCTTGGTCACTCTCCTGCCAGCCCTTGA 2836	
GC	CT	CTG	CTC	CTGG	TAC	CCCT	CTGGA	AC	CCATG	CTAAC	CTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCTC 2915	
TC	CT	TAG	CTG	CTCCCC	AG	ACTGT	CTGGG	CCATCT	GGG	GATC	AGGG	AGAGGCAGGAGTACTGACGAGGCAG 2994
TG	AC	CT	GAG	CTGAT	CA	ACC	CAG	AG	CA	CC	AG	AGTCTACAGTGGCTGGCTCAGCTCCTATGGGAGGCC 3073
TAC	AG	GGG	TACT	TAAG	CTAG	GGG	GTCA	TCTCAT	TTT	GATCT	GG	AAAGGCTACAGGCTCCTGATGTGAAGACAGGCC 3152
CA	CT	AC	ATA	AGA	AG	CCACT	GGA	AT	AG	ACTG	AC	AGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231

Fig.1H

CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCTAAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310  
ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCTGTCTCTTCCT 3389  
ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGTGCGAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468  
TGCCACCGCTCCTTTTGCTGTGGCCCTGGCACAGCCCCAACACTGCAGGGCCCCACCTTCTCTCTTGGGGGTAGGGACAC 3547  
ATAAGGAAACCTAACCCACCTCCAAACAACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626  
CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCCTGCCTG 3705  
GAGCATAGGGGTAAGCCGAGGAGAGCAGCCCTCAGAGACATCAGCTAAACATAGGTGCCCTATGTCCCTCCCT 3784  
TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGTCTTCATCCTCTCCCACATCAGCAAGGATAGGGCT 3863  
GCGGCTGCCCTAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
AAAGCTCTTGAAGATCAAAAGCTCTGGCGGTACAGCTGTCTGGCCTGTGGCCAGCCCATGGGATGTGCTGGCCAG 4021  
GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCCTCGCTGGCTGACACTATCA 4100  
GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGATGGCTCCAGA 4179  
CTCTGTACGCCCTCTGCAGGGCCACACAAGTCTCCGAGCCAAAGTCCACAAGCCTCCATGGTTCCTGGCTCCTCCT 4258  
GTGGAGTGCTCCTGTTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATTGGTCCCTTGT 4337  
GTCTCTGTTTACTGTCCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGCTGGGAGTGGGGTGATGCT 4416  
GGCTGACCCCCACCTGGTCTGCCAACAGAACCTGGGGCCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495  
ACACTGGCCAGGCTGAGTGGGCAGAGCAACAAGTGGAAGGGATCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574  
AGATCCAGCGAGGAGTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCCCTCCAGCAG 4653  
GGATATGACTTTGGACAACAAGGCTTTATTTGTAATAATGCTCTTAATATGCAACTTTGAGAATAAGATAGAAACATCA 4732  
TGTATTTTAAATATAAATGAAGTGTGACACACTGTATACAATTTAATATATAATTTTAGGATTTTGTATTAAAGAA 4811  
AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATTCTCA 4890  
TTGTTGTAGAAAAAATAAAAAAAGGGCGGCGCGC 4928

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Fig.11



	10	20	30	40	50	60	70
Hum.	MAPPAARLALLSAAALTLAARPA	PSPGLGP	CEFTANG	ADYRGTQ	NWTALQG	GKPCLF	WNETFQHPYNT
	.....	.....	.....	.....	.....	.....	.....
Mur.	MAPPAARLALLSAAALTLAARPA	PGPR--	SGPEC	TANGADYRGTQ	SWTALQG	GKPCLF	WNETFQHPYNT

[illegible]

	150	160	170	180	190	200	210
Hum.	SNKLT	IQTCTCISFCRSQRFKFAGMESGYACFCGNNPDYWKYGEEASTECSVCFGDHTQPCGGDGRIILFD					
	:	:	:	:	:	:	:
Mur.	SNKLT	IQTCTCISFCRSQRFKFAGMESGYACFCGNNPDYWKHGEAASTECSVCFGDHTQPCGGDGRIILFD					
	140	150	160	170	180	190	200

	220	230	240	250	260	270	280
Hum.	TLVGACGGNYSAMSSVVYSPDFD	TYATGRVCYWTIRVPGASHIHFS	PLFDIRDSADMVELLDGYTHRV				
	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::
Mur.	TLVGACGGNYSAMAAVVYSPDFD	TYATGRVCYWTIRVPGASRIHFN	FTLFDIRDSADMVELLDGYTHRV				
	210	220	230	240	250	260	270



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Fig. 1L

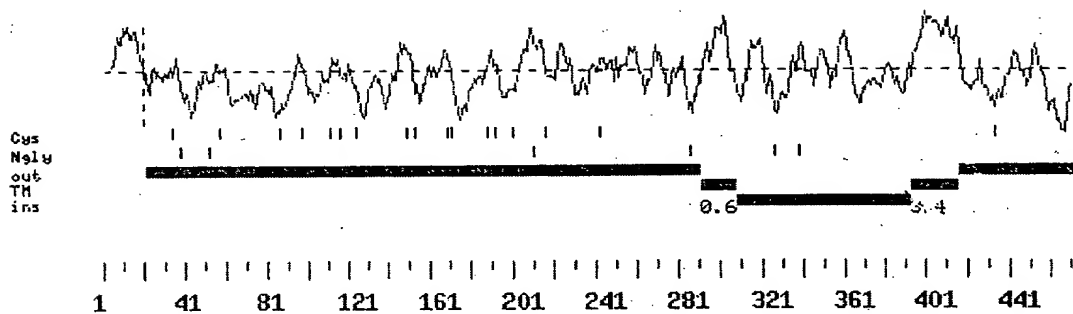
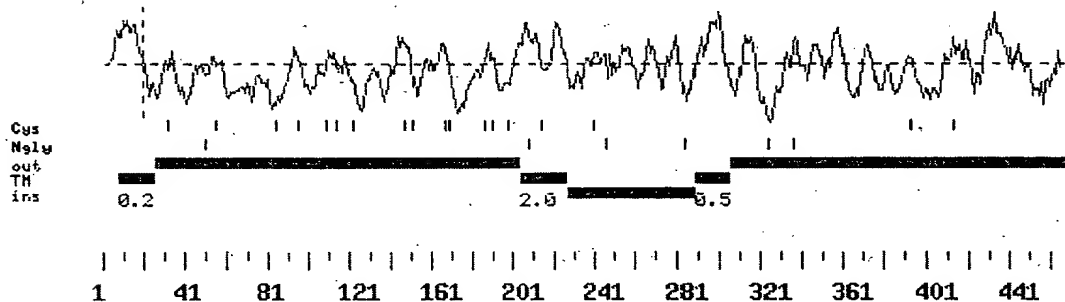


Fig. 1M



GCGGCCGCTCGGATCTAGAACTAGTA	M	M	L	P	Q	N	S	W	H	I	D	F	G	13
ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA														66
R C C C H Q N L F S A V T C I L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTA ACT TGC ATC CTG CTC CTG AAT														126
S C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q A V T R H G K I W L D														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG														486

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Fig. 2A

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 2B

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

Fig. 2C

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

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Fig. 2D

G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	TCT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

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Fig. 2E



C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

Fig. 2F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	CAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

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Fig. 2G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

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Fig. 2H

C L K R E D P H G T R T S D D T P N H G 1433  
TGC CTC AAG AGA GAG GAC CCA CAT GGG ACA AGA ACC TCA GAT GAC ACC CCC AAC CAT GGT 4326

C E D A S D T S L L L G V L P A S E A T K 1453  
TGT GAA GAT GCT AGC GAC ACA TCG CTG TTG GGA GTT CTT CCT GCC TCT GAA GCC ACA AAA 4386

\*  
TGA 1454  
4389

CTTTAGACTTCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACACAACCTTTTAAATGAATAAAGAGGA 4468  
AGTCAAGTTGCCCTATGGAAAACCTTGCCAAATAACATTTCTTGAACAATAGGAGAACACAGCTAAATTGATAAAGACTGG 4547  
TGATAATAAAAAATTGAATTATGTATATCATCTGTTAAAAAAAACAAAAAAGAAAAACGACCGTGGGTCG 4626  
AC 4628

Fig. 2I

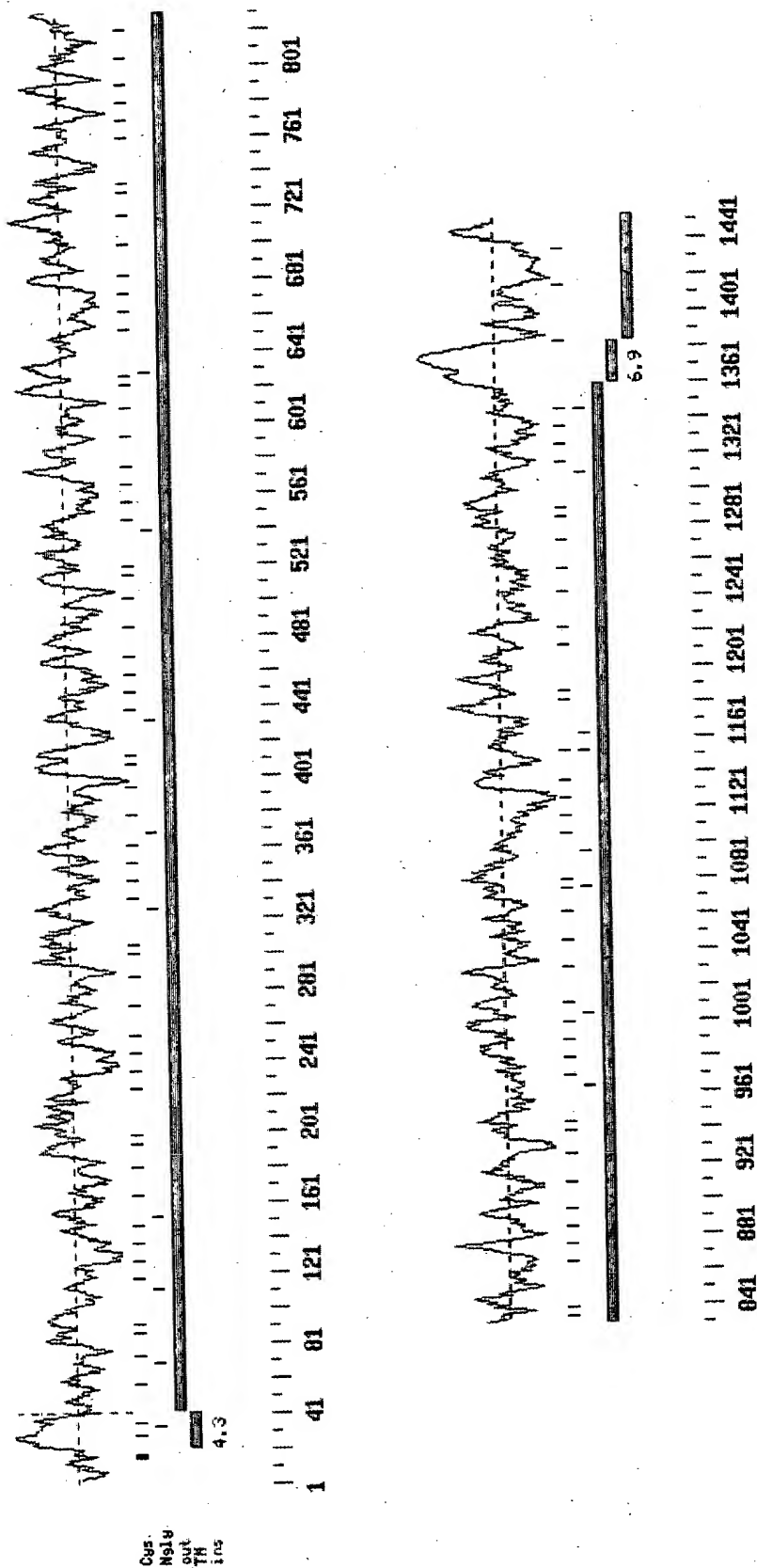


Fig. 2J

Hum.	10	20	30	40	50	60	70
	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNSCFLISSFNGTDLELRVLVNGDGPCSGTVEVKFQGWG						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	10	20	30	40	50	60	70
	MAL-----GR---HLSRLGL---CVLLLTGT--MVG---GQALELRCLKDGVHRCEGRVEVKHQGEWG						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Hum.	80	90	100	110	120	130	
	TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH---REWGSHN						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	60	70	80	90	100	110	
	TVDGYRWTLKDASVVCRCQLGCGAAIG-FPGGAYFGPLGPIWLLYTSCEGTSTVSDCEHSNIKDYRNDG						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Hum.	140	150	160	170	180	190	200
	CYHGEDVGVNCYGEANLGLRLVDGNNSCSCGRVEVKFQERWGTICDDGWNLTAAVVCRCQLGCPSSFISG						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	120	130	140	150	160	170	180
	YNHGRDAGVVCSG----FVRLAGGDGPCSCGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Hum.	210	220	230	240	250	260	270
	VNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTTCYDSSDLELRVLVGGTNRCMGRVE						
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	190	200	210	220	230	240	250
	HELFPRESSAQVWAEFRCEGEPELWVCPRPVPCPGGTCHHSGSAQVVCASAYSEVRL-MTNGSSQCEGQVE						

Fig. 2K

Hum.	280	290	300	310	320	330	340
	LKIQRWGT	CHHKWN	AAADVCK	QLCGGTAL	HFAGLPH	LQSGSDV	VWL
	...	...	...	...	...	...	...
WC1	MNISQWRAL	CASHW	SLANAN	VICRQL	CGGVA	ISTPG	PHLVE
	260	270	280	290	300	310	320
Hum.	350	360	370	380	390	400	410
	VNFDCLH	QNDV	SVICSD	GADLEL	RLADGS	NNCSGR	VEVRI
	.	...	...	...	...	...	...
WC1	GGPDCSH	GN	TASVICS	GNQI	-----	QVLPQC	ND
	330	340					350
Hum.	420	430	440	450	460	470	480
	FGSRRAK	PSNEAR	DIWINS	ISCTG	NESALW	DCTYD	GKAKR
	...	...	...	...	...	...	...
WC1	-----	SQPTG	SA-----	ASEDSA	-----	PY-----	CSDSR
		360					370
Hum.	490	500	510	520	530	540	550
	GRLEVKY	QGEW	GTVCH	DRWSTR	NAAVV	CKQLG	CGKPM
	...	...	...	...	...	...	...
WC1	GRVEILD	QGSW	GTICDD	GWDLDD	ARVVCR	QLGCC	EALNAT
	390	400	410	420	430	440	450

Fig. 2L

560	570	580	590	600	610	620	
Hum.	HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCGRLEVFYFQGRWGTVCDDGWNKAAAVVCSQLDC						
	.....	.....	.....	.....	.....	.....	
WC1	SRGWQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGVCVRNPMEDITVSTICRQLGC						
460	470	480	490	500	510	520	
630	640	650	660	670	680	690	
Hum.	PSSIIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCNSGWNDCSHSEVDGVICSDASDMELRLVGG						
	..	..	..	..	..	..	
WC1	GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSLWQCPSPDPWNNYNSCSPKEEAYIWCADSR--QIRLVDGG						
530	540	550	560	570	580	590	
700	710	720	730	740	750	760	
Hum.	SRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL						
	.....	.....	.....	.....	.....	.....	
WC1	GRCSGRVEILDQGSWGTICDDRWDLDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV						
600	610	620	630	640	650	660	
770	780	790	800	810	820	830	
Hum.	WDCIRWEWKQTACHLNMEASLICSABHRQPRVLVGADMPGCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL						
	:	:	:	:	:	:	
WC1	WRCPSWGRQHCNHQEDAGVICSGF--VRLAGDGPGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL						
670	680	690	700	710	720	730	

Fig. 2M



840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWA	EFQCEGSETHALCPIVQH	PEDTCIHSREVGVC	SRYT	DVRLV-NG	
	:: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVAAEFRC	DGGEPELWSC	PRVPCGGTCLHSGAAQV	CVSVTEVQ	LMKNG
	740	750	760	770	780	790 800
910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWSL	CDTHWDPEDARVLC	RQLSCGTALSTTG	GKYIGERSVRVW	GHRF	CHLGNESL
	:: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	TSQCEGQVEMKISGRWR	ALCASHWSLANANV	VCRLGCGVAIST	PRGPHLVEGDQ	ISTAQFHCS	GAESF
	810	820	830	840	850	860 870
980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPCI	HGNTVSVICTGSLTQ	PLFPCLANVSDPYLS	AVPEGSALICLED	KRLRLVDG	DSRC
	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	LWSCPVTALGGPDC	SHGNTASVICS	GNHTQVLPQCND	FLSQPAGSAASEE	SSPYCSDSR	QLRLVDGGGPC
	880	890	900	910	920	930 940
1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYH	DGF	WTICDDG	WDLSDAHVVC	QKLGCGVAFNATV	SAHFGE
	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	GGRVEILDQGS	WTICDD	WDLD	DDARVVC	RQLGCC	EALNATGSAHF
	950	960	970	980	990	1000 1010

Fig. 2N

```

1120      1130      1140      1150      1160      1170      1180
Hum. PSRGWQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWSVGRNRNITTAIAGIVCRQLG
      :::::::::::::::::::: : : :::::::::::::::::::: : : ::::::::::::::::::::
WC1 PSRGWGRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWSVCRSPMEDITTVSVICRQLG
      1020      1030      1040      1050      1060      1070

1190      1200      1210      1220      1230      1240
Hum. CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSA PWERRISSPAEETWITCEDR-----
      ::::: . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPGPKYSSCSPKEEAYISCEGRRPKSCPTAAA
1080      1090      1100      1110      1120      1130      1140

1250      1260      1270      1280      1290      1300
Hum. -----IRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAEAEVVCQQLGCGSALALRDASFQGTGTIW
      .:::::::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : :
WC1 CTDREKLRLRGDSECSGRVEVWHNGSWGTVCDSDWSLAEAEVVCQQLGCGQALEAVRSAAFPGNGSIW
1150      1160      1170      1180      1190      1200      1210

1310      1320      1330      1340      1350      1360
Hum. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCG-----QSLKSLNASSGHLALI
      ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNSLPGFSLPGVLC LI
1220      1230      1240      1250      1260      1270      1280

```

Fig. 20

```

1370      1380      1390      1400      1410
Hum. LSSIFGLLLVLFILFTWCRVQK-----QKHLPRLVS-----TRRRG-----SLEENLFHEME
      :... :...: . :: : .. : ... :
WC1 LGSLFLVLVIIVTQLLRW-RAERRALSSYEDALAEAVYEELDYLITQKEGLSPDQM TDVPDENYYDDAE
1290     1300     1310     1320     1330     1340     1350

Hum. TC-----LKREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLG V
      . : :...::..... : : : ..... : :...
WC1 EVPVPGTPSPSQGNEEEVPEKEDGVRSSQTGSFLNFSREAA NPGEESFWLLQGKKGDAGYDDVELSA
1360     1370     1380     1390     1400     1410     1420

      1450
Hum. LPASEAT-K
      : : : :
WC1 LGTSPVTFS
      1430
```

**Fig. 2P**



```

280      290      300      310      320      330      340
Hum.  TCCTTCGCCATGTTTCGTTTGGACAAGCCGTGA--CTAGACATGGAATAATTGGCTTGATGATGTTTC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GCCATTG--GTTTTCCTGGAGGGGCTTATTTGGGCCAGGACTTGGCCCCCATTTGGCTTTTGTATACTTC
220      230      240      250      260      270      280
      350      360      370      380      390      400      410
Hum.  CTGTTATGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAATGGGGAAGCCATAACTGTTATCAT
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   ATGTGAAGGGACAGAGTCAACTGTCAGTGACTGTGAGCAT-TCTAATATTAAGAC-TATC-GTAATGAT
290      300      310      320      330      340      350

420      430      440      450      460      470      480
Hum.  GGAGAAGATGTTGGTGTGAACGTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GGCTATAATCATGGTCGGGA---TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360      370      380      390      400      410      420

490      500      510      520      530      540      550
Hum.  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GAC-CCTGCTCAGGGCGAGTAGAAGTGCATT--CTGGAGAAGCTTGGATCCCAAGTGT-CTGATGGGAACT
430      440      450      460      470      480

```

Fig. 2Qiii

```

560      570      580      590      600      610      620
Hum.  ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGATGTCCATCTTTTATTCTTCTGGAGTTGT
      .. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TCACACTTGCCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG
490      500      510      520

630      640      650      660      670      680      690
Hum.  TAATAGCCCTGCTGTATTGCGCCCCATTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TTGTGGC-----AAGGCTG--TGTCTGT-----CCTGGGACATGAG-----CTCTT
530      540      550      560

700      710      720      730      740      750      760
Hum.  CTGGAATTGCAGACATCGTGGATGGGGAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CAGAGAGTCCAGT-GCC-----CAGGCTG--GGC----TGAAGAGTTCA-----GG
570      580      590      600

770      780      790      800      810      820      830
Hum.  TATGATAGTAGTATCTTGAACCTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGAGAGTAGAGCTGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TGTGAGGGGGAGGAGCCTGAGCT-----CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-
610      620      630      640      650

```

Fig. 2Qiii

	840	850	860	870	880	890	900
Hum.	AAATCCAAGGAGTGGGGACCGTATGCCACCATAAGTGAACAATGCTGCAGCTGATGTCGTATGCAA						
	:::	:::	:::	:::	:::	:::	:::
WC1	-----TCCA-----GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
	660	670	680	690	700		
	910	920	930	940	950	960	970
Hum.	GCAGTTGGGATGTGGAACCGCACTTCACCTTCGCTGGCTTGCCTCATTTCAGCTCAGGGTCTGATGTTGTA						
	::	::	::	::	::	::	::
WC1	ACT-----CAGAAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT						
	710	720	730	740	750	760	
	980	990	1000	1010	1020	1030	1040
Hum.	TGGCTTGATGGTGTCTCCTGTCTCCGGTAATGAATCTTTTGGACTGCAGACATTCGGAAACCGTCA						
	:::	::	::	::	::	::	::
WC1	GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-CTGGAGTCTGGCCCAATGCC---A						
	770	780	790	800	810	820	
	1050	1060	1070	1080	1090	1100	1110
Hum.	ATTTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTGGAACTGCGACT						
	::	::	::	::	::	::	::
WC1	ATGTTATCTGTCGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT						
	830	840	850	860	870	880	

Fig. 2Qiv

```

1120      1130      1140      1150      1160      1170      1180
Hum. AGCAGATGGAAGTAACAATTGTTTCAGGGAGAGTAGAGGTGAGAATTCA-TGAACAGTGGTGGACAATATG
   .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCGATTTCACCTGCTCTG---GGGC-----TG
      890      900      910      920      930

1190      1200      1210      1220      1230      1240      1250
Hum. TGACCAGAACTGGAAGAATGAACAAGCCCTTGTTGTTGTAAGCAGCTAGGATGTCCGTTCAGCGTCTTT
   .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 AGTCCT-TCCTGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGGTCCCTGACTGTTTCCCAT
      940      950      960      970      980      990

1260      1270      1280      1290      1300      1310      1320
Hum. GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTGGGATAAACAGCATATCTTGCACTGGG
   .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GGCAACACAGCCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCAGTGCAACGA-CTCCG--
      1000     1010     1020     1030     1040     1050     1060

1330      1340      1350      1360      1370      1380      1390
Hum. AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAGCAAGCAAGCAACATGCTTCCGAAGATCAGATG
   .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 --TGTCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG
      1070     1080     1090     1100
```

Fig. 2Qv



	1400	1410	1420	1430	1440	1450	1460
Hum.	CTGGAGTAATTGTTCTGATAAAGGCAGATCTGGACCTAAGGCTTGTGGGGCTCATAGCCCCCTGTATGG						
	:: ...	::	::	::	::	::	::
WC1	CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG---GACGGGG--GC--GGTCCCTGCGCCCGG						
	1110	1120	1130	1140	1150	1160	
	1470	1480	1490	1500	1510	1520	
Hum.	GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGACTGTGTGTCATGACAGATGGAGCACAAGG-AATGC						
	:::: ::	::::	::::	::::	::::	::::	::::
WC1	GAGAGTGGAGATCCTTGACCAAGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC						
	1170	1180	1190	1200	1210	1220	
	1530	1540	1550	1560	1570	1580	1590
Hum.	A-GCTGTTGTGTAAACAATTGGGATGTGGA-AAGCCTATGCATGTGTTGGTATGACCTATTTTAAAG						
	:: ::	::	::	::	::	::	::
WC1	CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG						
	1230	1240	1250	1260	1270	1280	1290
	1600	1610	1620	1630	1640	1650	1660
Hum.	AAGCATCAGGACCTATTGGCTGGATGACGTTTCTTGCAATGGAAATGAGTCAAATATCTGGGACTGTGA						
	:: ::	::	::	::	::	::	::
WC1	CAGGATCAGGGCCCATCTGGTTGGACAACCTTGAACCTGCACAGGAAAGAGTCCACGTGTGGAGGTGCC						
	1300	1310	1320	1330	1340	1350	1360

Fig. 2Qvi

```

1670      1680      1690      1700      1710      1720      1730
Hum. ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TTCCCGGGGCTGGGGCAGCACAACTGCAGACACAAGCAGGACGCGGGGTCTCTGCTCAG--AGTTC-
1370      1380      1390      1400      1410      1420      1430

1740      1750      1760      1770      1780      1790      1800
Hum. ACATGGGGCCTGAGGCTGGTGGCGGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTCAAGGAC
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 -CT--GGCCCTCAGGATGGTGAGTGAGGACCAGCAGTGCTGGTGGCTGGAAGTTTCTACAATGGGA
1440      1450      1460      1470      1480      1490      1500

1810      1820      1830      1840      1850      1860      1870
Hum. GGTGGGCACAGTGTGTGATGACGGCTGGAACAGTAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CCTGGGGCAGTGTCTGCCGTAACCCCATGGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
1510      1520      1530      1540      1550      1560      1570

1880      1890      1900      1910      1920      1930      1940
Hum. CCCATCTTCTATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAAAAATTGGCTCGATG
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 T--GGGGACAGTGGAAACCCCTCAACTCTTCTGTGCTCTTAGAGAAGGTTTAGGCCACAGTGGGTGAT-
1580      1590      1600      1610      1620      1630

```

Fig. 2Qvii

	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGTG--GGGAAATAATGAC						
	.....	.....	.....	.....	.....	.....	.....
WC1	-AGATCCAGTGTCCGAAACTGACACCTCTCT---CTGGCAGTGTCCCTCTGACCCCTTGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGAGCTGAGGCTGTGGG						
	:: ::	.....	:: ::	.....	:: ::	:: ::	.....
WC1	T-CATGCTCTCCAAGGAGGAAGCCTATATCTGTTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGAAGCAGCAGGTGTGCTGGAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT						
	.....	:: ::	.....	.....	.....	:: ::	.....
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCAACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGGAATGAACATTGCTGAAGTTGTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA						
	.....	.....	.....	.....	.....	.....	.....
WC1	CGCTGGGACCTGGACGATGCCCGTGTGTTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA						
	1840	1850	1860	1870	1880	1890	1900

Fig. 2Qviii

**Fig. 2Qix**

2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TTAAATTGTGGAGATGCCATATCTCTTCTGTGGGAGATCACTTTGGAAAAGGG-AAATGG				
	.....	.....	.....	.....	.....	.....
WC1	GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCTGGGACACATGCCATTTCAGAGAGTCCGATGG					
2180	2190	2200	2210	2220	2230	2240
2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGAGTGAAACTCACCTTGTCATTATGCCCCATTGTTCAA					
	....	.....	.....	.....	.....	.....
WC1	CCAGGTCCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGGAGCCTGAGCTCTGGTCCTGCCCCCAGAGTGCCCC					
2250	2260	2270	2280	2290	2300	2310
2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACTTGATCCACAGCAGAGAGATTGGAGTTGTCTGTTCCTCCGATATACAGATGTCCGAC					
	.....	.....	.....	.....	.....	.....
WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTTCAGTGTACACAGAAAGTCCAGC					
2320	2330	2340	2350	2360	2370	2380
2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAATCC---CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC					
	.....	.....	.....	.....	.....	.....
WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC					
2390	2400	2410	2420	2430	2440	2450

Fig. 2Qx

	2780	2790	2800	2810	2820	2830	2840
Hum.	TGTGTACACCCACTGGGACCCAGAAGATGCCCGTGTTC	TATGCAGACAGCTCAGCTGTGGGACTGCTCT					
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	TCTGTGCCCTCCCACTGGAGTCTGGCCAAATGTTGTCTGT	CGTCAGCTCGGCTGTGGAGTCGCCAT					
	2460	2470	2480	2490	2500	2510	2520
	2850	2860	2870	2880	2890	2900	2910
Hum.	CTCAACCACAGGAGGAAAATATATTGGAGAAAGAAGTGTTC	GTGTGGGACACAGGTTTCATTGCTTA					
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	CTCCACCCCAAGAGGACACACTTGGTGGAGGAGGTGATCAGATCT	CAACAGCCCAATTTCAGTCTCA					
	2530	2540	2550	2560	2570	2580	2590
	2920	2930	2940	2950	2960	2970	2980
Hum.	GGGAATGAGTCACCTTCTGGATAACTGTCAAATGACAGTTCTT	GGAGCACCTCCCTGTATCCATGGAAATA					
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	GGGGCTGAGTCCTTCCTGTGGAGTTGTCCTGTGACTGCCCTT	GGGTGGCCCTGACTGTTCCCATGGCAACA					
	2600	2610	2620	2630	2640	2650	2660
	2990	3000	3010	3020	3030	3040	3050
Hum.	CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTT	CCATGCCCTCGCAAATGTATCTGACCC					
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	CAGCCCTCTGTGATCTGCTCAGGAAACCAACCCAGGTGCTG	CCCCAGTGCAACGACTTCCTGTCTCAACC					
	2670	2680	2690	2700	2710	2720	2730

Fig. 2Qxi

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTC	CAGAGGGCAGTGCTTT	GATCTGCTTAGAGGACA	AAACGGCTCCGCCTAGTGGAT			
	.	.....	.....	.....	.....	.....	.....
WC1	TGCAGGCTCTGCGGCCT	CAGAGGAGAGTTCTCC	CTACTGCTCAGACAGCAG	CGCTCCGCCTGGTGGAC			
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGTGCC	GGGAGAGTAGAGATCTAT	CACGCGGCTTCTGGGGC	ACCATCTGTGATGACG			
	.....	.....	.....	.....	.....	.....	.....
WC1	GGGGCGGTCCCTGCGGC	GGGAGAGTGGAGATCCT	TGACCAAGGCTCCTGGG	CACCATCTGTGATGATG			
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCGATG	CCCACTGGTGTCAAAAG	CTGGGCTGTGGAGTGGC	CTTCAATGCCACGGT			
	.....	.....	.....	.....	.....	.....	.....
WC1	ACTGGGACCTGGACGAT	GCCCCGTGTGGTGTGC	AGGCAGCTGGGCTGTGG	AGAAGCCCTCAATGCC	ACGGG		
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTGGGG	AGGGTCAAGGCCCATCT	GGCTGGATGACCTGAAC	TGCACAGGAACGGAGTCC			
	.....	.....	.....	.....	.....	.....	.....
WC1	GTCTGCTCACTTCGGGG	CAGGATCAGGGCCCATCT	GGCTGGACGACCTGAAC	TGCACAGGAAGGAGTCC			
	2950	2960	2970	2980	2990	3000	3010

Fig. 2Qxiii

```

3340      3350      3360      3370      3380      3390      3400
Hum.  CACTTGTGCAGTGCCCTTCCCGCGGCTGGGGGCAGCACGACTGCAGGCACAAGGAGGACGCGGGGTCA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  CACGTGTGGAGGTGCCCTTCCCGGGCTGGGGCGGCACGACTGCAGACACAAAGGAGGACGCGGGGTCA
3020      3030      3040      3050      3060      3070      3080

3410      3420      3430      3440      3450      3460      3470
Hum.  TCTGCTCAGAATTACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  TCTGCTCAGAGTTCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA
3090      3100      3110      3120      3130      3140

3480      3490      3500      3510      3520      3530      3540
Hum.  AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACCCAGCCATAGCAGGCATTGTG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  GGTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCAGCCCCCATGGAAGATATCACTGTGTCCCGTGATC
3150      3160      3170      3180      3190      3200      3210

3550      3560      3570      3580      3590      3600
Hum.  TGCAGGCAGCTGGGCTGTGGGAGAATGGAGTTGTACAGCCTCGCCCCCTTA--TCT-AAGACAGGCTCTG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTGTGGTCTCAGGGAAGGTTCTA
3220      3230      3240      3250      3260      3270      3280

```

Fig. 2Q<sup>iii</sup>



```

3610      3620      3630      3640      3650      3660      3670
Hum. GTTTCATGTGGGTGGATGACATTGAGTGTCTTAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GACCCCGGTGGTAGATTAAATTCAGTGTCTCGGAAATGGATACCTCTCTCTGGCAGTGTCTTCTGCCCC
3290      3300      3310      3320      3330      3340      3350

3680      3690      3700      3710      3720      3730      3740
Hum. ATGGGAGCGAAGAAATCTCCAGCCCCAGCAGAGACCTGGATCACATGTGAAGATAGAATA---AGAG-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 ATGGAAATACAGTTCATGCTCTCCAAGGAGGAGGAGCCTACATCTCATGTGAAGGAAGAACCCCAAGAGC
3360      3370      3380      3390      3400      3410      3420

Hum. -----TGC-----GTGGAGGAGACACCGAGTGTCTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TGTCCAACTGCTGCCGCTGCACAGACAGAGAGAAGCTCCGCCCTCAGGGGAGGAGACAGCGAGTGTCTCAG
3430      3440      3450      3460      3470      3480      3490

3770      3780      3790      3800      3810      3820      3830
Hum. GGAGAGTGGAGATCTGGCAGCAGGCTCCTGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GCGGGGTGGAGGTGTGGCACACAACGGCTCCTGGGGCACCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
3500      3510      3520      3530      3540      3550      3560

```

Fig. 2Qxiv

```

3840      3850      3860      3870      3880      3890      3900
Hum.  GGAAGTGTGTGTCAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTGGCCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  TGAGTGGTGTGTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGCTGCGGTCTGCAGCATTTGGCCCT
3570      3580      3590      3600      3610      3620      3630

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAGTGAACCATCTGGTTGGATGACATGCGGTGCAAGGAAATGAGTCATTTCTATGGGACTGTCACG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGAATGGGAGCATCTGGCTGGACGAGGTGCAGTGCAGGCGCGGAGTCCTCCCTGTGGGACTGTGTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGG---ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGAGCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGGAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTATCCA
      : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  AACATTGCCCCACGACCACAGCAGGGACCAGAACCAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

```

Fig. 2Qxv

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4100      4110      4120      4130      4140
Hum. G-----TATCTT---TGGGCTC-CTTCTC---CTGGTTCT-----GTTTATTCTATTCTCA
:      :      :      :      :      :      :      :      :      :
WC1 GGGGTTCTCTGCCTTATCCTGGGGTCGCTTCTCTCCCTGGTCCTCGTCATCCTGGTGACTCAGCTACTCA
3850      3860      3870      3880      3890      3900      3910

4150      4160      4170      4180
Hum. CGTGGTG--CCGAGTTCAGAAACAAAAACATCT-----GCCC---CT---CAGAGTTT-----
:      :      :      :      :      :      :      :      :      :
WC1 GATGGAGAGCAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
3920      3930      3940      3950      3960      3970      3980

4190      4200      4210      4220
Hum. -----CAAC-----CAGAAAGGAGGG---GTTCT-CTCG---AGGAGAAATTATCCATGA-----
:      :      :      :      :      :      :      :      :      :
WC1 CGATTACCTTCTGACACAGAAAGGAAGGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCCTGATGAAAAAT
3990      4000      4010      4020      4030      4040      4050

4230      4240      4250
Hum. ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
:      :      :      :      :      :      :      :      :      :
WC1 TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACCTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060      4070      4080      4090      4100      4110      4120

```

Fig. 2Qxvi

```

4260      4270      4280      4290
Hum. CCACATGGGACAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  CCCCAGAGAAGGAGGACGGGTGAGGTCTCTCAGACAGGCTCTTTCTGAAC TTCTCCAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

      4300      4310      4320      4330
Hum. ----CCATGGTT--GTGAAGA----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: . . :::::
WC1  TAATCCTGGGAAGGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

      4340      4350
Hum. CTT-----CCTG-----CCTCTGAAGCCACAAA
      :: :::: ::::: ::::: ::::: . . .
WC1  GTTGAAC TCAGTCCCCTGGGAACATCCCCAGTGACTTTCTCTCG
4270      4280      4290      4300

```

Fig. 2Qxvii

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	12
													67
L L G L F L F L Q L L Q L L L L P T T A G	CTC	CTG	GGC	CTT	TTC	CTC	TTC	CAA	CTG	CTG	CTG	CCG	ACG
													32
													127
G G G Q G P M P R V R Y Y A G D E R A	GGA	GGC	GGG	CAG	GGG	CCC	ATG	AGG	GTC	AGA	TAT	GCA	GGG
													52
													187
L S F F H Q K G L Q D F D T L L L S G D	CTT	AGC	TTC	TTC	CAC	CAG	AAG	GGC	CTC	CAG	GAT	TTT	GAC
													72
													247
G N T L Y V G A R E A I L A L D I Q D P	GGA	AAT	ACT	CTC	TAC	GTG	GGG	GCT	CGA	GAA	GCC	ATT	CTG
													92
													307
G V P R L K N M I P W P A S D R K K S E	GGG	GTC	CCC	AGG	CTA	AAG	AAC	ATG	ATA	CCG	TGG	CCA	GCC
													112
													367
C A F K K K S N E T Q C F N F I R V L V	TGT	GCC	TTT	AAG	AAG	AAG	AGC	AAT	GAG	ACA	CAG	TGT	TTC
													132
													427
S Y N V T H L Y T C G T F A F S P A C T	TCT	TAC	AAT	GTC	ACC	CAT	CTC	TAC	ACC	TGC	GGC	ACC	TTC
													152
													487
F I E L Q D S Y L L P I S E D K V M E G	TTC	ATT	GAA	CTT	CAA	GAT	TCC	TAC	CTG	TTG	CCC	ATC	TCG
													172
													547

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Fig. 3A

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	1087

Fig. 3B

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

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Fig. 3C

S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	48 / 96
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	632
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	1927
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	652
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	1987
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	672
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	2047
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	692
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	2107
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	712
																				2167

Fig. 3D



R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R	732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA	2227
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D	752
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC	2287
N	N	C	L	G	T	E	V	A	*											762
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317
ACT	CTA	GGC	ACAG	GGCG	GTG	CGGT	GCAG	GCAC	CTGG	CCCAT	GTCT	GGCT	GGCG	GGCC	CAAG	CAC	AGCC	CTG	ACT	2396
TG	AC	AG	CAG	CAC	AAAG	ACCA	CTTT	CTCCCC	TGAG	AGAG	CTTCT	GTCT	ACTCT	GTG	CATC	ACTG	ATG	CAC	ACT	2475
TG	AT	GC	AC	AG	CAG	CTG	CTGCC	CTAT	GG	ACTCC	CTTCT	ACCA	AG	CAC	ATG	AGCT	CTCT	AAC	AGG	2554
CC	AG	AC	CT	GT	CTAC	ACTG	ATATT	GAA	GAAC	CTGG	AGAG	ATCCT	TCA	GTTC	TGG	CCAT	TCC	AGG	ACCC	2633
CAC	AG	TG	TT	CA	AG	ATCC	TAAAA	AAAC	CTGC	CTGT	CCCC	AGG	ACCC	TATG	GTAA	TGA	ACAC	CCAA	CAAT	2712
AT	AT	GT	AA	CA	AT	GC	CACT	CTCC	AACT	CTGA	AGCT	GGCG	TTTG	GAC	ACCA	CACT	CCCT	TCT	CCC	2791
TGC	AG	GA	TC	GT	CCCT	CTG	CTT	ACCA	GTCC	GTGC	ACCG	CTG	ACT	CCC	AGGA	GTCT	TCT	CTG	AGT	2870
AC	CT	TT	CT	TT	CA	GT	GGG	GC	AG	ACT	CTG	ATCCC	CTT	GT	CCCC	TGG	CAG	GGG	TAA	2949
TC	AC	TC	TT	TA	CCCT	TA	CCCT	CT	CCCC	CTCC	CTT	TC	CTT	TTG	GAT	TTC	AG	AA	AACT	3028
AG	AG	ACT	GT	TT	TTT	TTAT	TAAAA	ATATA	AAG	CTT	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3104

Fig. 3E

Hum.	10	20	30	40	50	60	70
	MALPALGLDPWSLLGLFLFQLLQLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQFLPLPSLPASGTGGQGPMPRVKYHAGDGHRALESFFQKGLRDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY						
	.....	.....	.....	.....	.....	.....	.....
Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNPGLPRLKNMIPWPASERKKTECAFKKKSNETQCFNFIRVLVSYNATHLY						
	.....	.....	.....	.....	.....	.....	.....
Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLLPISEDKVMEKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLLPLIDKVMGKGQSPLTFTSTQAVLVDGMLYSGTMNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Hum.	220	230	240	250	260	270	280
	TLGSQPVLKTDFLRWLHHDASFVAIIPSTQVVYFFFEETASEDFFERLHTSRVARVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....
Mur.	220	230	240	250	260	270	280
	TLGSHPVLKTDFLRWLHADASFVAIIPSTQVVYFFFEETASEDFFEELYISRVAQVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....

Fig. 3F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAV						
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLLMDEHVVGTPLLVKSGVEYTRLAV						
Hum.	430	440	450	460	470	480	490
	ETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGA VFGFSGGVW						
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLPDSEPVRLQLAPAQGA VFAFGSGGIW						
Hum.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCTCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQS						
Mur.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCLLSGST-KPWKQDMERGNPEWVCTRGPMA RSPRRQS						

Fig. 3G

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLI	VQDGVGGLYQCWATENG					
	.....	.....	.....	.....	.....	.....	.....
Mur.	560	570	580	590	600	610	620
	PPOLIKEVLTVPNSILELRCPHLSALASYWWSHG	GRAKISEASATVYNGSLLLPQDGVGGLYQCVATENG					
	.....	.....	.....	.....	.....	.....	.....
Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWPHFVT	VLFAVLGALI					
	.....	.....	.....	.....	.....	.....	.....
Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGASMAAQSYWPHFLI	VTVLLAIVLLGVLT					
	.....	.....	.....	.....	.....	.....	.....
Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASD	VDADNNCLGTEVA					
	.....	.....	.....	.....	.....	.....	.....
Mur.	700	710	720	730	740	750	760
	LLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHRTSASD	VDADNNHLGAEVA					
	.....	.....	.....	.....	.....	.....	.....

Fig. 3H

Fig. 31

Fig. 31

	530	540	550	560	570	580	590
Hum.	GGAGGACAAGGTCA	TGAGGGAAAGGCCA	AAGCCCCCTT	GACCCCGCTC	ACAAGCATACG-G	CTGTCTT	
	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	
Mur.	GATAGACAAGGTCA	TGACGGGAAGGCCA	AAAGCCC-TTT	GACCCTGTTCA	CAGCACACAAGCT	GTCTT	
	560	570	580	590	600	610	620

	600	610	620	630	640	650	660
Hum.	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	TTCCTGGCAGTGAGCCCATCCTGATGCGCAC	A				
	:::	:::	:::	:::	:::	:::	:::
Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC	TTCCTGGCAGCGAGCCCATCCTGATGCGGACA					
	630	640	650	660	670	680	690

	670	680	690	700	710	720	730
Hum.	CTGGGATCCCAGCCTGTCTCAAGACCGACA	ACTTCTCCGCTGGCTGCATCATGACGCC	TCTTTGTGG ::: ::: ::: ::: ::: ::: ::: :::				
Mur.	CTGGGATCCCATCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGGGATGCC	TCTTCCTTG 700 710 720 730 740 750 760					

	740	750	760	770	780	790	800
Hum.	CAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCGAGGACAGCCAGCGAGTTGACTTCTTTGA						
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	CAGCCATTCCCATCCACCAGGTCGTCTATTCTTCTTGAGGACAGCCAGCGAGTTGACTTCTTTGA						
	770	780	790	800	810	820	830

Fig. 3K

Fig. 3L



	1090	1100	1110	1120	1130	1140	1150
Hum.	GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	GGGAAGTACAAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCCGA						
	1120	1130	1140	1150	1160	1170	1180
	1160	1170	1180	1190	1200	1210	1220
Hum.	GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	GGCCAGGCAGTTGCTCCCATGTGGCCCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTCCTGAT						
	1190	1200	1210	1220	1230	1240	1250
	1230	1240	1250	1260	1270	1280	1290
Hum.	GGATGAGCAAGTGGTGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	GGATGAGCACGTGGTAGGAACACCCCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG						
	1260	1270	1280	1290	1300	1310	1320
	1300	1310	1320	1330	1340	1350	1360
Hum.	ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTCATGTACCTGGGAACCAACACAGGTCGCTCCACA						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TCAGCTCGGGCCTTGATGGGAGCAGCCCATGTGTCATGTATCTGGGTACCTCCACGGTCCCTGCACA						
	1330	1340	1350	1360	1370	1380	1390

Fig. 3M

	1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGTTAAGTGGGGACAGCAGTGTCTCATCTGTTGGAAGAGATT	CAGCTGTTCCCTGACCTGAACC					
	::::::::::::	:	::::::::::::	::::	::::::::::::	::::::::	::::::::
Mur.	AGGCTGTGTTGCCCTCAGGACACAGTGTCTTATCTGTGGAGGAGATT	CAGCTGAGCCCTGACTCTGAGCC					
	1400	1410	1420	1430	1440	1450	1460

	1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTCGCAACCTGCAGCTGGCCCCACCCAGGTGCAGTGT	1450	1460	1470	1480	1490	1500
	TTGTAGGCTTCTCAGGAGTGTCTGGAGG						
	.....						
Mur.	TGTTCGAAACCTGCAGCTGGCCCCCGCCAGGGTGCAGTGT	1450	1460	1470	1480	1490	1500
	TTGCAGGCTTCTCTGGAGGCATCTGGAGA						
	1470	1480	1490	1500	1510	1520	1530

[illegible]

	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGACCCCTGAGTCCC	GAACTGTTCCTCCTG	TCTGCCTGAACCTG	AACCTGAACTCCTG	GAAAGCAGGACAT		
	:	:	:	:	:	:	:
Mur.	CCTGGACCCCTGAATCA	AGACTCTGCAGCCTT	CTGTCTGGCTC-TACC	AAGCCT--TGGAAGC	AGGACAT		
	1610	1620	1630	1640	1650	1660	1670

File 3N

	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC						
	1680	1690	1700	1710	1720	1730	1740
Mur.	GGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGCCCCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCC						
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCATTAAGAAGTCCTGGTGTCGCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTCTCAG						
	1750	1760	1770	1780	1790	1800	1810
Mur.	CCTCAACTAATTAAGAAGTCCTGACAGTCCCCCAACTCCATCCTGGAGCTGGCGTGGCCCCCACCTGTCTCAG						
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCTCTTATTATTGGAGTCATGGCCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG						
	1820	1830	1840	1850	1860	1870	1880
Mur.	CACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAATCTCAGAAGCCTCTGTCTACCGTCTACAATGG						
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGTGGGCAACTGAGAAATGGCTTT						
	1890	1900	1910	1920	1930	1940	1950
Mur.	CTCCCTCTTGCTGCTGCCGACGATGGTGTCTGGGGCCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC						

Fig. 30

[illegible]

File 3P

```

2210      2220      2230      2240      2250      2260      2270
Hum.  GGGAGAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Mur.  GGGAAAAGGCTCCACTGAGCAGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA
2240      2250      2260      2270      2280      2290      2300

2280      2290      2300      2310      2320      2330      2340
Hum.  TGTGACGCTGACAACAACACTGCCACTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Mur.  CGTAGATGCCGACACAACAACCATCTGGCGCCGAAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC
2310      2320      2330      2340      2350      2360      2370

2350      2360      2370      2380      2390      2400      2410
Hum.. GGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGATGACAGCAGCAAAA
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Mur.  AGAGCAAGCCACTGGCCTTGTGGCTATGC----CAGGCACAG-----TGCCACTCT--
2380      2390      2400      2410      2420

2420      2430      2440      2450      2460      2470      2480
Hum.  AGACCACCTTTCTCCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Mur.  -GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-----C
2430      2440      2450      2460
```

Fig. 3Q



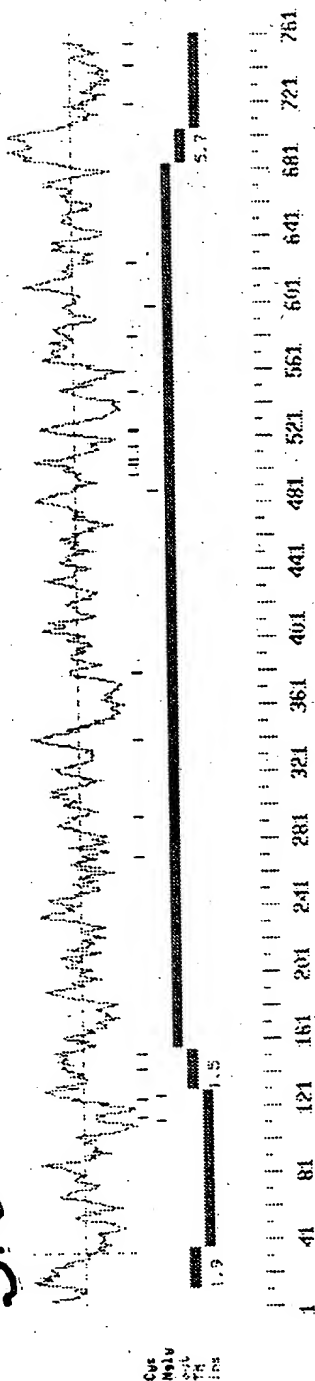
	2760	2770	2780	2790	2800	2810
Hum.	----GCTGCCGCTTTGGACACCAACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC					
	2730	2740	2750	2760	2770	2780
Mur.	AGCAGCTGCTGCTTTGAACACACAGCCCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT					
	2820	2830	2840	2850	2860	2870
Hum.	TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACTTTCTTCTTGC					
	2800	2810	2820	2830	2840	2850
Mur.	TTCCCTTACCAGTCGGGCCATACTGTTT--GGGAAGTCACTCTGAAGTCTAACCACTTCTCTCTTG					
	2890	2900	2910	2920	2930	2940
Hum.	TTCAGTTGGGCAGACTCTGATCCCT--TCTGCCCTGGCAGAAATGCAGGGTAATCTGAGCCTTCTTC					
	2860	2870	2880	2890	2900	2910
Mur.	TTCAGTTGGACAGATTGTTATTGTTCTCTGCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTTC					
	2960	2970	2980	2990	3000	3010
Hum.	ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCCCTTTGTTTGGGATTCAGA					
	2930	2940	2950	2960	2970	2980
Mur.	---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC--TCCCTTTGTTTGGGATTCAGA					

Fig. 3S

**Fig. 3T**



Fig. 3U



GTCGACCCACGCGTCCGCGGACGCGTGGGACGGCTCCCGGCTGCAGTCTGCCCCGCCCGCGGGGCCGAGTC	79
GCGAAGCGCGCCTGCGACCCGCGTCCGGCGCGCTGGAGAGGACGCGAGAGCC	152
K V A A L L L G L L L E C T E A K K H C	6
AAG GTG GCG GCG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC	212
W Y F E G L Y P T Y Y I C R S Y E D C C	46
TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT	272
G S R C C V R A L S I Q R L W Y F W F L	66
GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGC TTT CTT	332
L M M G V L F C C G A G F I R R R M Y	86
CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC	392
P P P L I E E P A F N V S Y T R Q P P N	106
CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT	452
P G P G A Q Q CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	126
CCC GGC CCA GGA GCC CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	512
M N P V G N S M A M A F Q V P P N S P Q	146
ATG AAC CCT GTC GGG AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG	572

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Fig. 4A

G	S	V	A	C	P	P	P	A	Y	C	N	T	P	P	P	Y	E	166	
GGG	AGT	GTG	GCC	TGC	CCG	CCC	CCT	CCA	GCC	TAC	TGC	AAC	ACG	CCT	CCG	CCC	TAC	GAA	632
Q	V	V	K	A	K	*												173	
CAG	GTA	GTG	AAG	GCC	AAG	TAG												653	
TGGGGT	GTCC	CACG	TGCA	AGAG	GAGAC	AGGAG	GGCC	TTTCC	CTGG	CC	TTTCT	GTCT	TC	GT	TGAT	GT	CA	TTCC	732
GAACGG	TCTC	GTGG	CTGCT	AAGG	CAGT	TCCT	CTGAT	ATCCT	CACAG	CAAG	CACAG	CTCT	CTTT	TCAG	GC	TTTCC	ATGG	811	
AGTACA	ATAT	ATGA	ACTC	ACACT	TTTGT	CTCCT	CTGTT	CTCT	CTGTT	CTGAC	GCAG	CTCT	GTG	CTCT	CACAT	GGTAG	TGT	890	
GGTGAC	AGTCCC	GAGG	CTGAC	GTCC	TAC	GGTGG	CGTG	ACCA	GATCT	ACAG	GAGAG	AGACT	GTG	AGAG	GAAG	AGGC	CAG	969	
TGCTGG	AGGTG	CAGGT	GGCAT	GTAG	AGGG	CCAG	CCGAG	CATCC	CAGG	CAAG	CATC	CTTCT	GTCC	CCGG	TATTA	ATAGG	1048		
AAGCCCC	ATG	CCGG	GGCTC	AGCC	GATGA	AGC	AGCAG	CCGACT	GAGCT	GAGCCC	CAGC	AGTCA	TCTG	CTCC	AGCC	CTGT	1127		
CCTCTC	GT	CAGC	CTTCC	TCC	AGAG	CTGTT	GAGAG	ACATTC	AGAG	AGCA	AGCC	CTTGT	CATG	TTTCT	GTCT	1206			
CTGTTCA	TATC	CTAA	AGATAG	ACTT	CTC	CTG	CACCG	CCAGG	AAAGG	TAGC	ACGTG	CAGCT	CTCAC	CGAG	TGGGC	1285			
CTAGAA	TCAGG	CTTG	CCCTG	AGGC	CTGAC	AGTAT	CTGAC	ATCC	ACTA	AGCA	AAATTT	ATTT	AAAT	TCAT	GGAA	TCA	1364		
CTTCC	TGCCCC	AACTG	AGACAT	TGCAT	TTTGT	GAGCT	CTTGG	CTGAT	TTGG	AGAA	AGGACT	GT	TAC	CCAT	TTTTTT	1443			
GTGTG	TTTAT	GGAAG	TGCAT	GTAG	AGCG	TCC	TGCC	CTTGA	AAATC	AGACT	GGGTG	TGTCT	CCCT	GGAC	ATCA	CTGC	1522		
CTCTCC	AGGCAT	TTCT	CAGC	CCCG	GGGTCT	CCCT	CCCTC	AGG	CAGCT	CCAG	TGGT	GGTCT	CTGA	AGGG	TGCT	TTTCAA	1601		
ACGGGC	CACAT	CTGG	CTGG	AAGT	CACAT	GGACT	CTTCC	AGG	AGAG	AGAC	CAGCT	GAGG	CTCT	CTCT	GAGG	TTGT	1680		
GTTGGG	CTAAG	CGGG	TGTGT	GTCT	GGCT	CCAAG	GAGG	AGCT	TGCT	GGAA	AAAG	ACAG	GAAG	TACT	GACT	CAAC	1759		
TGCAC	TGAC	CATG	TTGT	CATA	ATTA	GAATA	AAAG	AAAG	AGTGG	TCGG	AAATG	CACAT	TCC	TGGA	TAGAA	TACAG	CTCA	1838	
CCCCAG	GATCT	CACAG	GATG	TCCT	GAGT	AGTTG	ACGG	CTAG	CGGG	GAGCT	AGTTCC	GGCC	CATAG	TTAT	AGTGT	TGA	1917		
TGTGT	GAAC	CGTG	ACCT	GTCC	GTGT	GCTA	AGAG	CTATG	CAGCT	TAGCT	GAGG	CCCTA	GAT	TACT	AGAT	GTGCT	GAT	1996	
CACGGG	GAATG	AGGTG	GGGTG	CTTAT	TTTT	TAATG	AACTA	ATCAG	AGCC	CTCTT	GAGAA	ATTTG	TACT	CA	TTGA	ACTGG	2075		
AGCATC	AAGAC	ATCT	CATG	GGAAG	TGGAT	ACGG	AGTGAT	TTTGG	TGTCC	ATGCT	TTTCA	CTCT	GAGG	ACAT	TTTA	ATCGG	GAG	2154	

Fig. 4B

AACCTCCTGGGGAATTTGTGGGAGACACTTGGGAACAAAAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233  
CCACCAAGTGCTCTGACCAACCTGGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGTCTGCAGGCCCTCCATCTAAA 2312  
TGAGACAACAAAGCACAAATGTTCACTGTTTACAACCAAGACAACACTGCGTGGTCCAAACACTCCTCTTCCTCCAGGTCA 2391  
TTTGTTTGGCAATTTTAAATGCTCTTTAATTTTTTGTAATGAAAAAGCACACTAAGCTGCCCTGGAAATCGGGTGCAGCTGA 2470  
ATAGGCACCCAAAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATTATGTTAAGAGACAGTATGGCTAGG 2549  
GCTCAACAATTTTGATTTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACCTTGGTTAGAATTGTGCTACTGT 2628  
GAACGCTGATCCTGCATATGGAAGTCCCACTTTTGGTGACATTTTCTGGCCATTCTTGTTCATTGTGTGGATGGTGGG 2707  
TTGTGCCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTAGAAATTCCTGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG 2786  
CAGATCTGTGCATGCTTTTCCCTCTGCAACAATTGGCTCGTTTCTCTTTTGTCTCTTTTGTATAGGATCCTGTTTCCT 2865  
ATGTGTGCAAAATAAAAAATAAATTGGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2944  
AAAAAAAAGGGCGGCGGC 2964

Fig. 4C

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GTCGACCCACGCGTCCGGCGCGCGTCTTCTGCGGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCGTCCCGGGGT 79  
  
GCGGACTGGCCCTGAGCTGGCCGTACAGCCCCGGCTTCGGACGGTCTCGCTGGAGCC ATG GGC CGC CGG CTC 151  
  
M G R R L 5  
  
G R V A A L L L L G L L V E C T E A K K H 25  
GGC AGG GTG GCG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 4D

C	W	Y	F	E	G	L	Y	P	T	Y	Y	I	C	R	S	Y	E	D	C	45
TGC	TGG	TAT	TTT	GAA	GGA	CTC	TAT	CCC	ACA	TAC	TAT	ATA	TGC	CGT	TCC	TAT	GAA	GAC	TGC	271
C	G	S	R	C	C	V	R	A	L	S	I	Q	R	L	W	Y	F	W	F	65
TGT	GGC	TCC	AGG	TGC	TGT	GTG	AGG	GCC	CTT	TCC	ATA	CAG	AGG	CTG	TGG	TAT	TTT	TGG	TTC	331
L	L	M	M	G	V	L	F	C	C	G	A	G	F	F	I	R	R	R	M	85
CTG	CTG	ATG	ATG	GGT	GTG	CTG	TTC	TGC	TGT	GGT	GCC	GGT	TTC	TTC	ATT	CGC	CGG	CGC	ATG	391
Y	P	P	P	L	I	E	E	P	T	F	N	V	S	Y	T	R	Q	P	P	105
TAT	CCG	CCA	CCA	CTC	ATT	GAG	GAG	CCC	ACA	TTC	AAT	GTG	TCC	TAT	ACC	AGG	CAG	CCA	CCA	451
N	P	A	P	G	A	Q	Q	M	G	P	P	Y	Y	T	D	P	G	G	P	125
AAT	CCT	GCT	CCA	GGA	GCA	CAG	CAA	ATG	GGA	CCG	CCA	TAT	TAC	ACC	GAC	CCT	GGA	GGA	CCC	511
G	M	N	P	V	G	N	T	M	A	M	A	F	Q	V	Q	P	N	S	P	145
GGG	ATG	AAT	CCT	GTT	GGC	AAT	ACC	ATG	GCT	ATG	GCT	TTC	CAG	GTC	CAG	CCC	AAT	TCA	CCT	571
H	G	G	T	T	Y	P	P	P	P	S	Y	C	N	T	P	P	P	P	Y	165
CAC	GGA	GGC	ACA	ACT	TAC	CCA	CCC	CCT	CCT	TCC	TAC	TGC	AAC	ACG	CCT	CCA	CCC	CCC	TAT	631
E	Q	V	V	K	D	K	*													173
GAA	CAG	GTG	GTG	AAG	GAC	AAG	TAG													655
CAAGATGCTACATCAAAGGCAAGAGGATGGACAGGCCCTTTTGTGTTACCTTCCCATCCTCACCAGATACTTGCTGATAG																				734

Fig. 4E

GGTGGTCCAAAGGAAAACTTGGATATTCTCAAAGCAAGCCAGCTCTCTTTCAAAGTCTTTTGTGGAGGACATTGAATC 813  
 CACACTGTCTCCTCTGTTGCTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCCTGAGGGTT 892  
 GATATTCCTAGGGTGTCCAGGTAGATCCTCGGAGAGAGGCTAAGGGAAAGGAAGCATAGCCTGTGTGTAGGGGG 971  
 CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTTCGAAGAGACACTATCCACCA 1050  
 TCCCAGCCCCATTCTCCTAATAAGAGCTGTGGGGCTGTGTTGTGATGCTCTTTTGGTCTCCACTCACATTTTGAAAAATAG 1129  
 GCTTTCCTCTGCAGGAATAGGAAAGACCCAAAGTACATAATTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCCTCAG 1208  
 TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATCTCTAAATGGAGACATT 1287  
 GCGTTTTATGAATCATCGTCTGGCTTTTCTTTTAGTGCAATGATTTGAAGTGAGGGTGTCCCTTTGAGATCAGATGGGGAG 1366  
 AGTGAACCTCTCGGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAAACACCCCTTTTCTTAGGTAGTTCTGGTGATGGGTT 1445  
 TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTTGACCCCTTGAGAGGAAGAGGACAGCCAAAG 1524  
 AAACTCAGCAAAAGCAAGACCAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGCCCTCA 1603  
 GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAAACCTACTTAGTTGCACAGATGACATAATCAAAAAGTAGAGAAAGAAG 1682  
 TGTAGTTAGAGATGCCATTTCACAGGTGAGAAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA 1761  
 TGGAGTTCTTTCCCTTGGCTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840  
 GGAAGTATAGCTAAGATGTCTAGATTATTTATATGTAGTATGGTGGGAGTGGGGCTGCAAGGAAGGGGCTGACATTG 1919  
 TAAATGAGAAAAATCAGAGCCATTGTATAAACTGTTACTTGTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT 1998  
 GAGTATTCCTTACCACCTACAAGACCAGGAGGCATGGTGTCTCTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAG 2077  
 GAATCGACAGTAGCTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG 2156  
 GGAAGGAAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCCTTGTGTCTCTGGC 2235  
 TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGTCCCTTGTGTTTACATAAGACACAAGACACAATGTCTGCTGTT 2314  
 TACAAATCAAGACGACTACATGGTCCAAACATTCTCTCTCTATCACTTGTGGCTTTAACTTCCATTTCCTCCGTT 2393  
 CCTTTTAAAAATCAAGAAGCACAGTCAGAGCTGCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC 2472  
 CATGACTAAATCTTATCTTTTGTATAGCAAAATCCTTTTAAGAAACTGAACAATTTGCTAAGGCTCAGCAATTTTATACTC 2551  
 CAATGTCTGTGAAGGTAAATTTTGTGTCATTTAGCCCAATTTGGAATTCCTTCTGACGTCAACACTGACAATGCSCT 2630  
 ATGGAAATTGCACTTCTGGGTATATGTCCAGCATCCTTGTGTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709

Fig. 4F

AGCTCTACTTCTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTTC 2788  
 TTGGCAACACTTGGCTCATATTCTTGTCTCTTTGATAGAGTCCTGTTTCCCTATGTATTTAAAAAATAATAAAGTG 2867  
 AATTAGTCAAAAAAATAAAAAAAGGCGGCCGC 2915

Fig. 4G

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLGLLLECTEAKKHCWFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	:	:	:	:	:	:	:
Mur.	MGRRLGRVAALLGLLVECTEAKKHCWFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	10	20	30	40	50	60	70
	80	90	100	110	120	130	140
Hum.	VLFCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPNPGFQAQQPGPPYYTD	PGGPMNPGNSMAMAFQV					
	:	:	:	:	:	:	:
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPNPAPGAQQMGPPYYTD	PGGPMNPGNTMAMAFQV					
	80	90	100	110	120	130	140
	150	160	170				
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK						
	:	:	:	:	:	:	:
Mur.	QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK						
	150	160	170				

Fig. 4H

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Fig. 4I

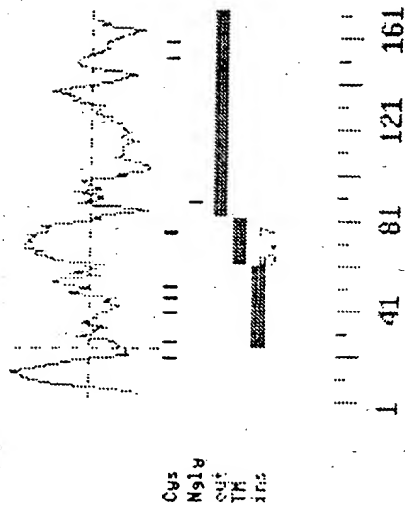
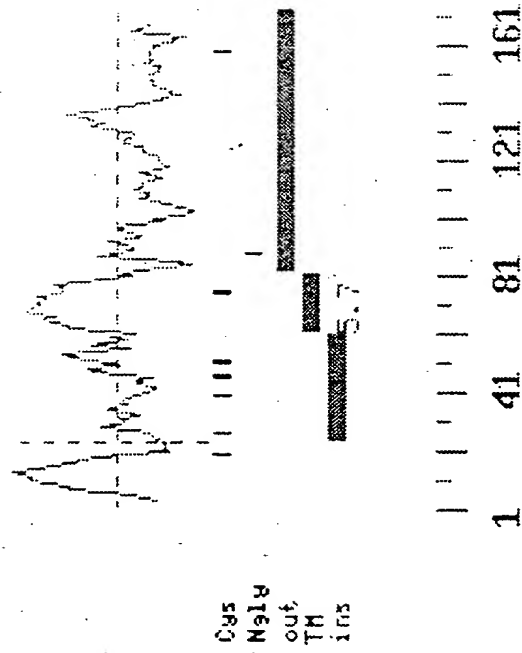




Fig. 4J



GTCGACCCACGGTCCGACGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
M C T K T I	
TCAAGAAAGGCCAGCACAGCAGAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
P V L W G C F L L W N L Y V S S S Q T I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GTT CAA GCT GGA	270
M K M I E Q M L K E K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

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Fig. 5A

L C P I I A S E V K A L N A N L S T L E	166
CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG	630
V L T K I D N Y T L L D Y S L I S S P E	186
GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA	690
I T E N Y L D L N L K G V F Y P L E N L	206
ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC	750
T D P P F S P V P F V L P E R S N S M L	226
ACC GAC CCC CCC TTC TCA CCA GGT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC	810
Y I G I A E Y F F K S A S F A H F T A G	246
TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG	870
V F N L T L S T E E I S N H F V Q N S Q	266
GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA	930
G L G N V L S R I A E I Y I L S Q P F M	286
GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG	990
V R I M A T E P P I I N L Q P G N F T L	306
GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG	1050
D I P A S I M M L T Q P K N S T V E T I	326
GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC	1110

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Fig. 5B

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTTGCAATTCA	CCCCCAGGAAGTAAATGGT	CTCTTAATCCTACAACTACTGTAA	ACCCAGAAAGACAGT	1579																
ACACACTGGAATTGTAAAG	CCCCCTTGTGAATTGCTTAGGCAGAAAGTTT	CTTTCTTAAGCCCTTCAGGAACCCAGAAATAA	1658																	
GGCAGACTCTGTAAAGGGATAA	ATAGAGGTGTCTGAATGTGAGTGATGCATGCTGCGTGTCTGTGTTATGTTG	1737																		
TTTGTGTTGTTGGGCAAGAA	GATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG	1816																		

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Fig. 5C

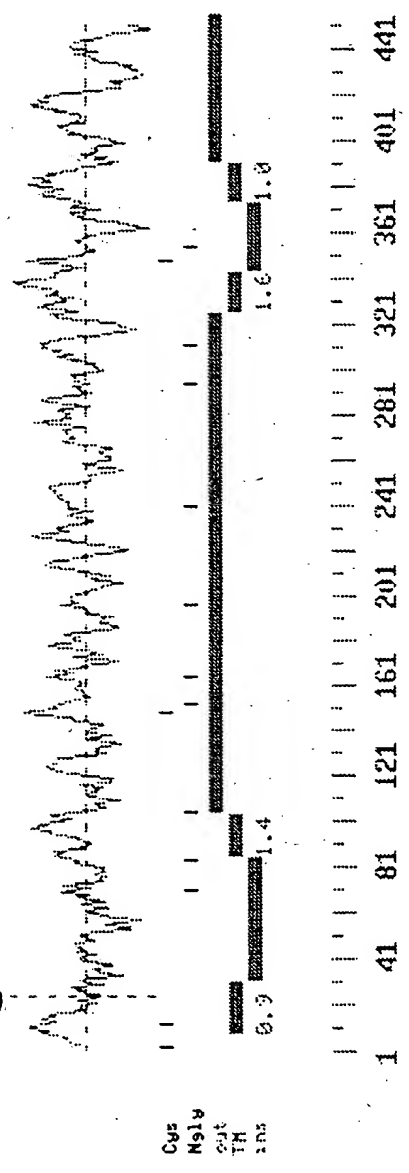
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ATGTTTATATTCACTGTTACTATCTTCTGTGTTTAAATTGTTTCTATCAAAAAAAAAAAAAAAAAAAGGGC 1974  
GGCCGC 1980

**Fig. 5D**

004250" E9084560

Fig. 5E



	10	20	30	40	50	60
286	MCTKT-IPVLWGCFL-LWNLVSSQTIYPGIKARITQALDYGVAQGMKMIQMLKEKKLPDLGSES					
	:	:	:	:	:	:
BPI	MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF					
	10	20	30	40	50	60
70	80	90	100	110	120	130
286	EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--					
	:	:	:	:	:	:
BPI	KIKHLGKGHSFYSDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRFLKMSGNFDLSIEGM					
	70	80	90	100	110	120
						130
286	-----KPI-----					
	:	:	:	:	:	:
BPI	SISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSVGWLIQLFHKKIESALRNKMNSQVCEKVTNS					
	140	150	160	170	180	190
						200
						210
						220
286	VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDNLKGVFYPLENLTDPFPFVFLPERSN					
	:	:	:	:	:	:
BPI	VSSKLQPYFQTLPMVMTKIDSVAGINYLVAAPPATTAETLDVQMKGEFFYSENHHNPPPPFAPPVMEFPAHD					
	210	220	230	240	250	260
						270

Fig. 5F

06-09-2008 17:00

230	240	250	260	270	280	290
286	SMLYIGIAEYFFKSASFAHFTAGVFNLTLS	STEEISNH--FVQNSQGLGNVLSRIA	EIYILSQPFMVRIMA			
	.....	.....	.....	.....	.....	.....
BBPI	RMVYLG	SDYFFNTAGLV	QEAGVLKMTLRD	DDMIPKESKFR	LTTKFFGTF	LPPEVAKKFP-NMKIQIHVSA
280	290	300	310	320	330	340

	300	310	320	330	340	350	360
286	TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTVGLVILGQRLVCSLSLNRFRALPE						
	. : : : : . : : : . : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : .						
BBPI	STPPHLSVQPTGLTTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRVLVGELKLDRLLELKH						
	350	360	370	380	390	400	410

	370	380	390	400	410	420	430
2286	SNRSNIEVLRFFENILSSILHFGVLPLANAKLQQGFPPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK						
	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :	:
BBPI	SNIGFPVELLDIMNYIVPILVLP RVNEKLQKGFP LPTPARVQLYNVVLPQHONFLFGADVVK----						
	420	430	440	450	460	470	480

286 QQPSFHVWEGNLIISQWRGKSAP 440 450

BPPI -----

Fin. 5G







GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATATGTGAAGAGTTTTTAAACCCACAAATCTTCTTACTTTAGA	79
M L E T L S R Q	
ATTAGTTGTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	8 149
W I V S H R M E M W L L I L V A Y M F Q	28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	209
R N V N S V H M P T K A V D P E A F M N	48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	269
I S E I I Q H Q G Y P C E E Y E V A T E	68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	83 / 96 329
D G Y I L S V N R I P R G L V Q P K K T	88
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	389
G S R P V V L L Q H G L V G G A S N W I	108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	449
S N L P N N S L G F I L A D A G F D V W	128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	509
M G N S R G N A W S R K H K T L S I D Q	148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	569

Fig. 6A

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168	
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629	
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188	
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689	
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208	
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749	
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228	
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809	
L	L	L	P	D	M	I	K	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869	
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268	
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929	
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288	
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989	
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308	
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049	
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328	
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109	

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Fig. 6B

L	E	K	C	N	Q	P	T	P	V	R	Y	R	V	R	D	M	T	V	P	348
CTG	GAA	AAA	TGC	AAT	CAG	CCA	ACT	CCT	GTA	AGG	TAC	AGA	GTC	AGA	GAT	ATG	ACG	GTC	CCT	1169
T	A	M	W	T	G	G	Q	D	W	L	S	N	P	E	D	V	K	M	L	368
ACA	GCA	ATG	TGG	ACA	GGA	GGT	CAG	GAC	TGG	CTT	TCA	AAT	CCA	GAA	GAC	GTG	AAA	ATG	CTG	1229
L	S	E	V	T	N	L	I	Y	H	K	N	I	P	E	W	A	H	V	D	388
CTC	TCT	GAG	GTG	ACC	AAC	CTC	ATC	TAC	CAT	AAG	AAT	ATT	CCT	GAA	TGG	GCT	CAC	GTG	GAT	1289
F	I	W	G	L	D	A	P	H	R	M	Y	N	E	I	I	H	L	M	Q	408
TTC	ATC	TGG	GGT	TTG	GAT	GCT	CCT	CAC	CGT	ATG	TAC	AAT	GAA	ATC	ATC	CAT	CTG	ATG	CAG	1349
Q	E	E	T	N	L	S	Q	G	R	C	E	A	V	L	*					424
CAG	GAG	GAG	ACC	AAC	CTT	TCC	CAG	GGA	CGG	TGT	GAG	GCC	GTA	TTG	TGA					1397
AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCCATGAAGGCAGAAATTACGGAGAGCA	1476																			
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTGGCACAATAATCCGACACTTACATTTTCTGTGATAA	1555																			
TTAAAGTACTTATTAGGTAATAAGAGGTTTTGTATGCTATTATATATCTCTTAAACACACCTATTGTTTTCTATAAGCCAT	1634																			
AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTAAACACACCTATTGTTTTCTATAAGCCAT	1713																			
ATTTTGGAGCACTAAAGTAAATGGCAAAATGGGACAGATATTGAGGCTGGAGTCTGTGGATTATTGTTGACTTGA	1792																			
CAAAATAAGCTAGACATTTTCACCTTGTGGCCACAGACACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA	1871																			
CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTTCTCAGAATAAGGCCAAGTTTATAGTTGCA	1950																			
TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAAAAAAAAA	2029																			
AAAAAGGGCGCGCGC	2044																			

85/96

Fig. 6C

	10	20	30	40	50	60	70
294	MLETLSRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIHQHGYPCEEYEVATEDG						
	:	:	:	:	:	:	:
HLP	M-----WLL---	LTMASLISVLGTTGHLFGKLH---	PGSPEVTMNISOMITYWGYPNEEYEVVTE	DG			
	10	20	30	40	50		
	80	90	100	110	120	130	140
294	YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK						
	:	:	:	:	:	:	:
HLP	YILEVNRIPYGKKNSGNTGQRPVFLQHGLLASATNWI	SNLPNNSLAFILADAGYDVWLGN	SRGNTWARR				
	60	70	80	90	100	110	120
	150	160	170	180	190	200	210
294	HKTLSIDQDEFWAFSYDEMAREDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKMYF						
	:	:	:	:	:	:	:
HLP	NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQQLHYVGH	SHSQGTTIGFIAFSTNP	SLAKRIKTFY				
	130	140	150	160	170	180	190
	220	230	240	250	260	270	
294	ALAPIATVKHAKSPGTFKFLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF						
	:	:	:	:	:	:	:
HLP	ALAPVATVKYTKSLINKLRFPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF						
	200	210	220	230	240	250	260

Fig. 6D

```
280      290      300      310      320      330      340
294 NTNNMNSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRLLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYNNVTAMNVPI
    270      280      290      300      310      320      330

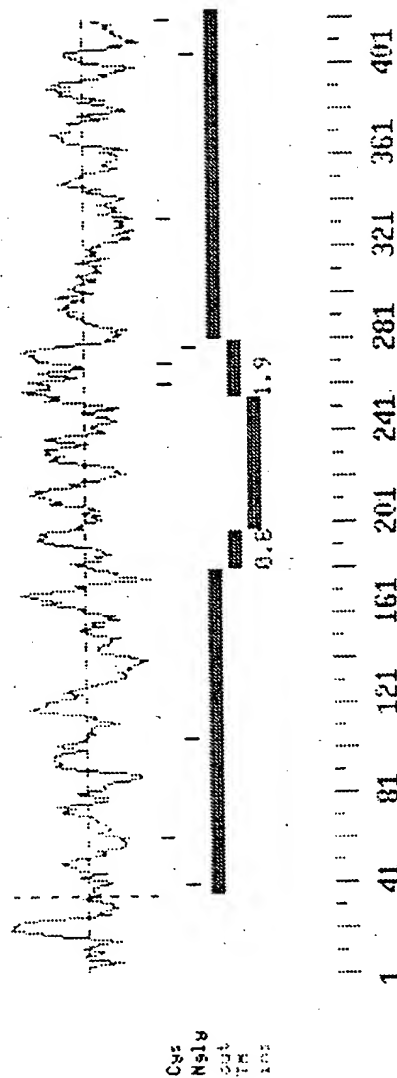
350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEI IHLMQQEETNLSQGRG
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
    340      350      360      370      380      390

420
294 EAVL

HLP ----
```

Fig. 6E

Fig. 6F



Cos  
Nslu  
out  
th  
inc



0967-8963 "0512-4000

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294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTK--AVDPEAFMNISEIIHQHGYPCPEEYEVATE
:      :::: . . . . :      :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCVLVWPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50      60

```

70	80	90	100	110	120	130
294	DGYILSVNRIPRGLVQPKKTGSRPVLLQHGLVGASNWIISNLPNNSLGFILADAGFDVWMGNSRGN	AW				
	::::: . . . . .					
LAL	DGYILCLNRI	PHGRKNHSDKGP	KPVFLQHGL	LADSSNWVTNL	ANSSLG	FILADAGFDVWMGNSRGT
	60	70	80	90	100	110 120

140	150	160	170	180	190	200
294	RKHKTLSDQDEFWAFSYDEMAREFDLPAVINFILQKTGQEKIYYVGYSQGTMTMGFIASFSTMPELAQIKIM					
	::					
LAL	RKHKTLVSQDEFWAFSYDEMAREFDLPAVINFILNKTGQEQVYYVGHVSQGTGTIGFIASFQIPELAKRIKM					
130	140	150	160	170	180	190

	210	220	230	240	250	260	270
2294	YFALAPIATVKHAKSPG	TKFLLPDMMIKLFGK	KEFLYQTRFLRQLVI	YLCGVILDQICS	NIMLLLG		
	.....	:: ::	:: ::	:: ::	:: ::	:: ::	:: ::
LLAL	FFALGPVASFCTSPMA	KLGRLPDHLIKDLFG	DKEFLPQSAFLKWL	GTHVCTHILKEL	CNLCFL	LCG	
	200	210	220	230	240	250	260

66  
Filing

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280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNIHLHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
:: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMLHWSQAVKFKQAFDQWSSAKNYFHYNQSYPTYNVKDMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNIEIHLMQQEEETNLSQGR
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LAL TAVWSSGGHDLADVVDVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

Fig. 6H

GTCGACCCACGGCTCCACGGGAGGGCTCCCGGGGCGAGCATTTGCCCCCCTGCACCACCTCACCAAG ATG GCT	75
T L G H T F P F Y A G P K P T F P M D T	22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC	135
T L A S I I M I F L T A L A T F I V I L	42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG	195
P G I R G K T R L F W L L R V V T S L F	62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC	255
I G A A I L A V N F S S E W S V G Q V S	82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC	315
T N T S Y K A F S S E W I S A D I G L Q	102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG	375
V G L G G V N I T L T G T P V Q Q L N E	122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG	435
T I N Y N E E F T W R L G E N Y A E E C	142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT	495
A K A L E K G L P D P V L Y L A E K F T	162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT	555

Fig. 7A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	CGG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 7B

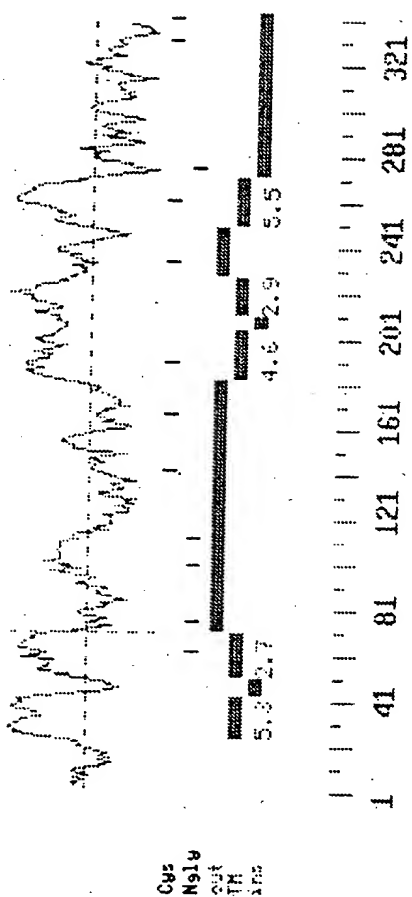
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TCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGTGACCTGCCTCATCACTGCCACCTAA 1891  
CGTCCCCCTGGGTGTTTCAGAAAAGATGCTAGCTCTGTAGGTCCCTCCGGCCTCACTAGAGGGCGCCCCCTATTACTC 1970  
TGGAGTCGACGCAGAGAATCAGGTTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCGAAGCTCATGA 2049  
GGACGTGCGACCCCGCGGAGAGCCATGAAAATTAAATGGGAAACACAGTTTATAAAAAAAAAGGGCG 2128  
GCGGC 2133

Fig. 7C

004250"E9082560

Fig. 7D



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10      20      30      40      50      60      70
296 MATLGHTFPFYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRKTRFLWLLRVVTSLFIGAAILAV
:  . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP M-RIAH-----ASSRGNI-----SIFSVELIPLIAYILILPGVR-RKRVTVTVTYVLMMLAVGGALIAS
10      20      30      40      50

296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL-----TGTPVQQLNETIN--YNEEFTW
. . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTCLKFERLLSSNDVLPGSDMTELYNEGEFDI
60      70      80      90      100      110      120

296 RLGENYAECAKALEKGLDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM
. . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP SGISSMAEALHHGLENGLPYPMLSVLEFYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCCLSVVLMFL
130     140     150     160     170     180     190

296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLTHHGPAP----WITLTGLLCVL
:  . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . :
CRP PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFTGENFERVDLTATFSFCFYLI FAIGILCVL
200     210     220     230     240     250     260

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Fig. 7E

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270      280      290      300      310      320
296 LGLAMAVAHRMQPHRLKAFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
      :::::  . . . : :::::  :  :::  :  :::  :::  . . .
CRP CGLGLGICEHWRIYTLSTFLDASLDLDEHVGPWKKLPTGGPALQGVQIGAYGTNTTNSRRDKNDISSDKTA
      270      280      290      300      310      320      330

      330
296 STKAY-----CK-----EAHPKDPD-----CA---L
      ..  ..  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
CRP GSSGFQSRSTSTCQSSASSASLRSQSSIETVHDEAELELERTHVHFLQEPCCSSSST
      340      350      360      370      380

```

Fig. 7F